

intro_stochastic_models

April 28, 2020

```
In [2]: import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import math
```

In this notebook, we begin by implementing some stochastic models using Gillespie's algorithms. The models are largely based on those given in the B5.1 Stochastic Modelling of Biological Processes (<https://courses.maths.ox.ac.uk/node/42068>) and Keeling's Modelling Infectious Diseases in Humans and Animals.

0.0.1 Stochastic Degradation

1. Set $t = 0$ and $A(t) = N$.
2. Generate a random number $r \sim \mathcal{U}(0, 1)$ and set $\tau = \frac{1}{kA(t)} \ln(\frac{1}{r})$.
3. If $t + \tau \leq t_{final}$, set $t = t + \tau$ and $A(t + \tau) = A(t) - 1$. If $A(t) > 0$ return to Step 2, otherwise exit.
4. If $t > t_{final}$, set $t = t_{final}$ and exit.

```
In [3]: def stochastic_degradation(A, t_final, k):
    t = 0
    A_hist = []
    t_hist = []
    while t <= t_final:
        r = np.random.rand()
        tau = math.log(1/r) / (k*A)
        t += tau
        A -= 1
        A_hist.append(A)
        t_hist.append(t)
        if A <= 0:
            break
    return t_hist, A_hist

# N = 20

t_hist_100, A_hist_100 = stochastic_degradation(20,30,0.1)

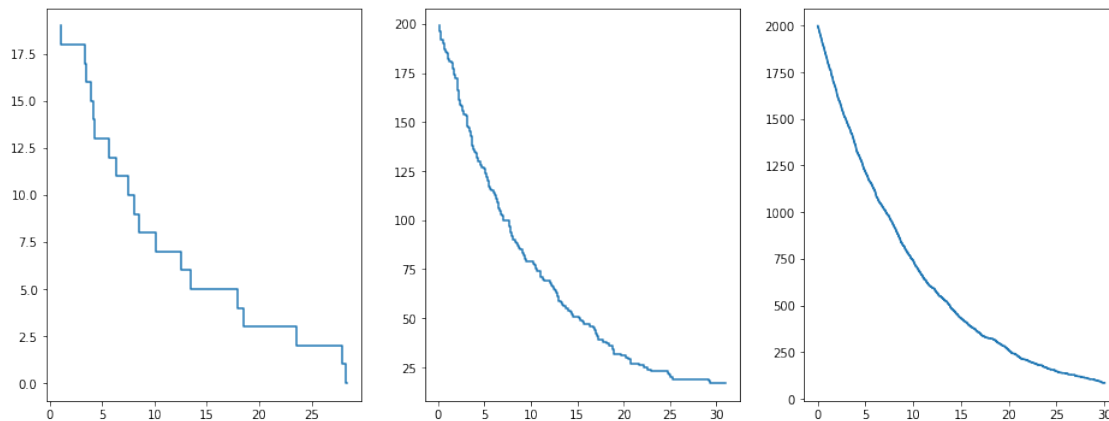
# N = 200
```

```
t_hist_1000, A_hist_1000 = stochastic_degradation(200,30,0.1)
```

```
# N = 2000
```

```
t_hist_10000, A_hist_10000 = stochastic_degradation(2000,30,0.1)
```

```
In [4]: f, (ax1, ax2, ax3) = plt.subplots(1, 3, figsize = (16,6))
ax1.plot(t_hist_100, A_hist_100, drawstyle = "steps-pre")
ax2.plot(t_hist_1000, A_hist_1000, drawstyle = "steps-pre")
ax3.plot(t_hist_10000, A_hist_10000, drawstyle = "steps-pre")
plt.show()
```

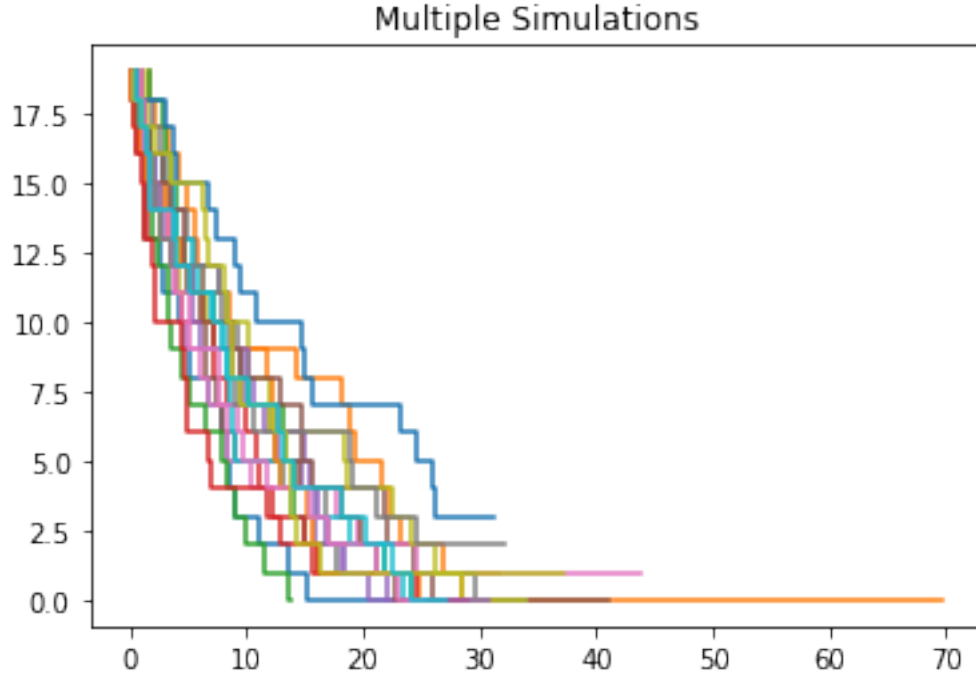


```
In [5]: # Computing the average among multiple simulations
```

```
t_mult_histories = {}
A_mult_histories = {}
for i in range(20):
    t_hist, A_hist = stochastic_degradation(20, 30, 0.1)
    t_mult_histories[i] = t_hist
    A_mult_histories[i] = A_hist
```

```
In [6]: f, ax = plt.subplots()
```

```
for i in range(20):
    plt.plot(t_mult_histories[i], A_mult_histories[i], drawstyle = "steps-pre")
plt.title("Multiple Simulations")
```



0.0.2 Chemical Master Equations

If we consider a biochemical network of N species, S_1, S_2, \dots, S_N , that may be involved in M possible reactions, R_1, R_2, \dots, R_M . We denote the population of species S_i at time $t > 0$ by its copy number $X_i(t)$ and define the state vector as

$$X_t = \begin{bmatrix} X_1(t) \\ X_2(t) \\ \vdots \\ X_m(t) \end{bmatrix}. \quad (1)$$

We also define the following state-change vector

$$v_j = \begin{bmatrix} v_{1,j} \\ v_{2,j} \\ \vdots \\ v_{N,j} \end{bmatrix} \quad (2)$$

where $v_{i,j}$ is the change in species i after the firing of reaction j . In this example, the following network containing two species A and B :



(7)

For the above four reactions, we therefore have the following propensity functions

$$a_1(t) = \frac{k_1}{\nu} A(t)(A(t) - 1) \quad (8)$$

$$a_2(t) = \frac{k_2}{\nu} A(t)B(t) \quad (9)$$

$$a_3(t) = k_3 \nu \quad (10)$$

$$a_4(t) = k_4 \nu \quad (11)$$

(12)

and the following state-change vectors

$$\nu_1 = \begin{bmatrix} -2 \\ 0 \end{bmatrix}, \quad \nu_2 = \begin{bmatrix} -1 \\ -1 \end{bmatrix}, \quad \nu_3 = \begin{bmatrix} +1 \\ 0 \end{bmatrix}, \quad \nu_4 = \begin{bmatrix} 0 \\ +1 \end{bmatrix}. \quad (13)$$

In [7]: `def gillespie_algo(t_final, A_0, B_0, k_rates):`

```
import numpy as np

def calc_a0(A, B, k_rates, return_all = True):
    a1 = calc_a1(A, B, k_rates[0])
    a2 = calc_a2(A, B, k_rates[1])
    a3 = calc_a3(A, B, k_rates[2])
    a4 = calc_a4(A, B, k_rates[3])
    if return_all:
        return a1+a2+a3+a4, [a1, a2, a3, a4]
    else:
        return a1+a2+a3+a4

def calc_a1(A, B, k):
    return k*A*(A-1)

def calc_a2(A, B, k):
    return k*A*B

def calc_a3(A, B, k):
    return k
```

```

def calc_a4(A, B, k):
    return k

def v1():
    return np.array((-2, 0))

def v2():
    return np.array((-1, -1))

def v3():
    return np.array((+1, 0))

def v4():
    return np.array((0, +1))

A = A_0
B = B_0
[k1, k2, k3, k4] = k_rates
t = 0
state_hist = []
t_hist = []

prop_fns = {0:v1, 1:v2, 2:v3, 3:v4}

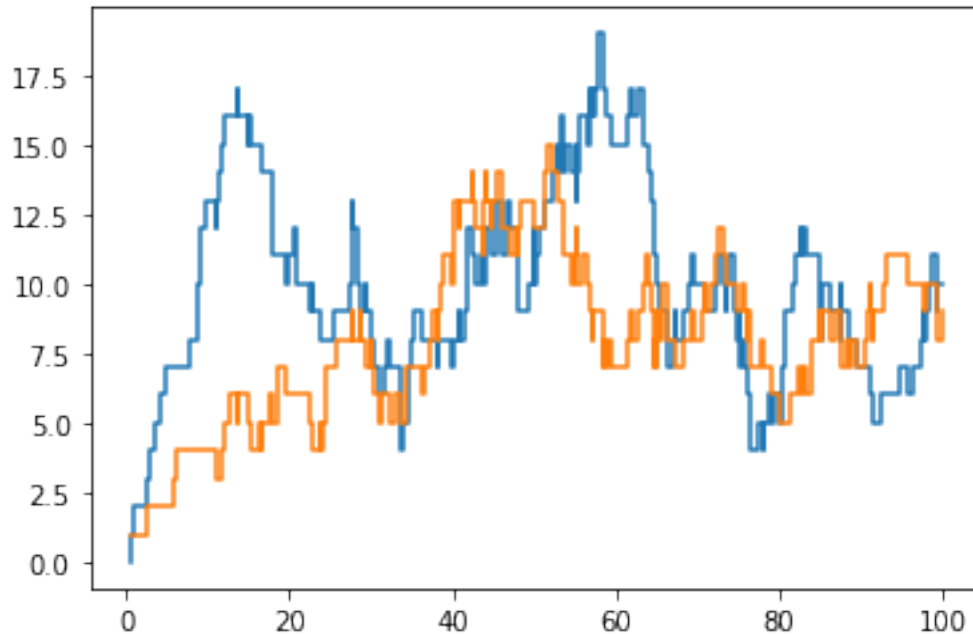
X = np.array((A, B))

while t <= t_final:
    # calculate a_0
    a_0, a_list = calc_a0(X[0], X[1], k_rates)
    # generate a reaction time
    r1 = np.random.rand()
    tau = math.log(1/r1) / (a_0)
    t += tau
    # choose a reaction
    r2 = np.random.rand()
    for idx in range(len(a_list)):
        #print("a_i: " + str(np.sum(a_list[:idx + 1])))
        if r2*a_0 < np.sum(a_list[:idx + 1]):
            reaction_idx = idx
            break
    elif idx == (len(a_list) - 1):
        reaction_idx = idx
    # update state vector
    X = X + prop_fns[reaction_idx]()
    state_hist.append(X)
    t_hist.append(t)
return t_hist, state_hist

```

```
In [12]: t_hist, state_hist = gillespie_algo(100, 0, 0, [0.001, 0.01, 1.2, 1.0])
```

```
In [13]: plt.plot(t_hist, state_hist, drawstyle = "steps-pre")  
plt.show()
```

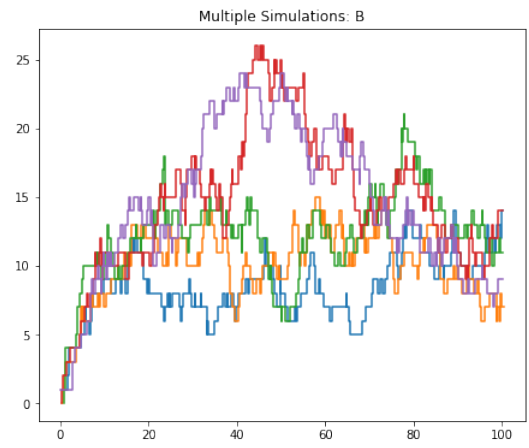
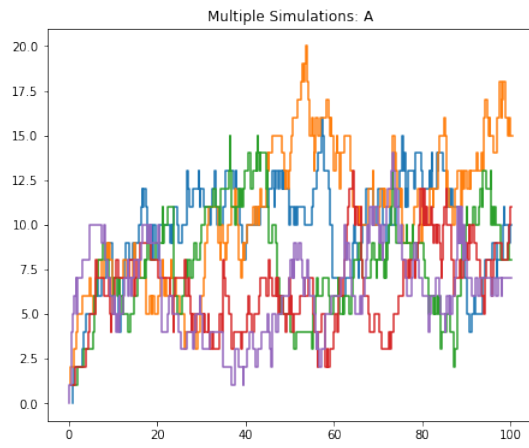


```
In [14]: # multiple simulations
```

```
t_mult_histories = {}  
A_mult_histories = {}  
B_mult_histories = {}  
  
for i in range(5):  
    time_hist, state_hist = gillespie_algo(100, 0, 0, [0.001, 0.01, 1.2, 1.0])  
    t_mult_histories[i] = time_hist  
    A_mult_histories[i] = [item[0] for item in state_hist]  
    B_mult_histories[i] = [item[1] for item in state_hist]
```

```
In [15]: f, (ax1, ax2) = plt.subplots(1,2, figsize = (16,6))
```

```
for i in range(5):  
    ax1.plot(t_mult_histories[i], A_mult_histories[i], drawstyle = "steps-pre")  
    ax1.set_title("Multiple Simulations: A")  
  
for i in range(5):  
    ax2.plot(t_mult_histories[i], B_mult_histories[i], drawstyle = "steps-pre")  
    ax2.set_title("Multiple Simulations: B")
```



In []: